Model building and refinement

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An abbreviated version of this protocol was published in Science in Aug 2022
Cryo-EM structure of the human IgM B cell receptor
DOI: 10.1126/science.abo3923

Detailed protocol

The sequence used for model building is the mIgM antibody.

The full-length mIgM sequence is listed below:

Heavy Chain:
MEFGLSWLFLVAILKGVQCQVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGKRPEWMGWLKPRGGAVNYARPLQGRVTMTRDVYSDTAFLEL

The heavy chain comprises three parts: synthetic signal peptide (10.1371/journal.pone.0116878), variable domain of VRC0 (10.1126/science.1192819), and constant domain of mIgM (Uniprot ID: P01871-2, https://rest.uniprot.org/uniprotkb/P01871-2.fasta). The three parts are highlighted by yellow, green and magenta color, respectively.
The codon optimized cDNA sequence:
ATGGAGTTCGGCCTGAGCTGGCTGTTCCTGGTGGCCATCCTGAAGGGGGTGCAGTGCCAAGTGCAGCTGGTGCAGAGCGGCGGGCAGATGAAGAAGCC

Light Chain:
MVLQTQVFISLLLWISGAYGGSDYKDDDDKGSPGDEVDAGEIVLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRW

The codon optimized cDNA sequence:
ATGGTGCTGCAGACCCAAGTGTTCATCAGCCTGCTCCTGTGGATCAGCGGCGCCTACGGCGGCAGCGACTACAAAGATGACGATGACAAGGGCAGCCC
The light chain comprises five parts: native signal peptide (Human Ig kappa chain V-IV region B17, https://doi.org/10.1038/nprot.2017.126), flag tag flanked by GS linkers, DrICE cutting site (10.1038/nsmb764), variable domain of VRC0 (10.1126/science.1192819), and constant domain of Igκ(Uniprot ID: P01834-1, https://rest.uniprot.org/uniprotkb/P01834.fasta). The five parts are highlighted by yellow, blue, red, green and magenta color, respectively.

How to cite:（Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used）

1. Su, Q. and Shi, Y. (2022). Model building and refinement. Bio-protocol Preprint. bio-protocol.org/prep2094.
2. Su, Q., Chen, M., Shi, Y., Zhang, X., Huang, G., Huang, B., Liu, D., Liu, Z. and Shi, Y.(2022). Cryo-EM structure of the human IgM B cell receptor. Science 377(6608). DOI: 10.1126/science.abo3923

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